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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=10; day=27; hr=8; min=42; sec=23; ms=108; ]

=====

\*\*\*\*\*

Reviewer Comments:

<210> 137

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> PDK1 - lys76 to ala

<400> 137

As an explanation of "Artificial Sequence", the above <223> response should only show "PDK1" (and, if possible, more information regarding the source of the genetic material). The "lys76 to ala" portion should go in its own <220>-<223> section.

<210> 138

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> Arg131 changed to alanine

The above <223> response is not a valid explanation of "Artificial Sequence"; please furnish a separate <220>-<223> section explaining "Artificial Sequence": please clearly indicate the source of the genetic material. Same type of error in Sequences 139-143.

\*\*\*\*\*

Application No: 10517225 Version No: 1.0

**Input Set:****Output Set:**

**Started:** 2009-10-09 19:08:43.555  
**Finished:** 2009-10-09 19:08:49.734  
**Elapsed:** 0 hr(s) 0 min(s) 6 sec(s) 179 ms  
**Total Warnings:** 32  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 143  
**Actual SeqID Count:** 143

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W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44)
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W 213	Artificial or Unknown found in <213> in SEQ ID (95)
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W 213	Artificial or Unknown found in <213> in SEQ ID (98)
W 213	Artificial or Unknown found in <213> in SEQ ID (99)
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W 213	Artificial or Unknown found in <213> in SEQ ID (101)
W 213	Artificial or Unknown found in <213> in SEQ ID (106)

**Input Set:**

**Output Set:**

**Started:** 2009-10-09 19:08:43.555  
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Error code

Error Description

This error has occurred more than 20 times, will not be displayed

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<110> ALESSI, Dario  
 BIONDI, Ricardo  
 KOMANDER, David  
 VAN, Aalten, Daan

<120> Methods

<130> ERP01.005APC

<140> 10517225

<141> 2009-10-09

<150> PCT/GB2003/002509

<151> 2003-06-09

<150> GB0213186.0

<151> 2002-06-08

<160> 143

<170> PatentIn version 3.1

<210> 1

<211> 4

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (2)..(3)

<223> Any amino acid

<400> 1

Phe Xaa Xaa Phe

1

<210> 2

<211> 6

<212> PRT

<213> Homo sapiens

<220>

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<222> (2)..(3)

<223> Any residue

<220>

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<222> (5)..(5)

<223> S or T

<400> 2

Phe Xaa Xaa Phe Xaa Tyr  
1 5

<210> 3

<211> 556

<212> PRT

<213> Homo sapiens

<400> 3

Met Ala Arg Thr Thr Ser Gln Leu Tyr Asp Ala Val Pro Ile Gln Ser  
1 5 10 15

Ser Val Val Leu Cys Ser Cys Pro Ser Pro Ser Met Val Arg Thr Gln  
20 25 30

Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly Gly Ser Arg Gln Gly  
35 40 45

Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser  
50 55 60

Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu  
65 70 75 80

Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val  
85 90 95

Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile  
100 105 110

Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr  
115 120 125

Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys  
130 135 140

Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser  
145 150 155 160

Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser

165

170

175

Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala  
180 185 190

Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro  
195 200 205

Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe  
210 215 220

Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn  
225 230 235 240

Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu  
245 250 255

Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile  
260 265 270

Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr  
275 280 285

Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr Asp Phe Pro Glu Lys  
290 295 300

Phe Phe Pro Lys Ala Arg Asp Leu Val Glu Lys Leu Leu Val Leu Asp  
305 310 315 320

Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu Gly Tyr Gly Pro Leu  
325 330 335

Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His Gln  
340 345 350

Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro Ala Met Ser Glu Asp  
355 360 365

Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu Leu Ser Gln Phe Gly  
370 375 380

Cys Met Gln Val Ser Ser Ser Ser Ser Ser His Ser Leu Ser Ala Ser  
385 390 395 400

Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn Ile Glu Gln Tyr Ile  
405 410 415

His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp Leu Gln Phe Ser Glu  
420 425 430

Asp Glu Lys Arg Leu Leu Leu Glu Lys Gln Ala Gly Gly Asn Pro Trp  
435 440 445

His Gln Phe Val Glu Asn Asn Leu Ile Leu Lys Met Gly Pro Val Asp  
450 455 460

Lys Arg Lys Gly Leu Phe Ala Arg Arg Arg Gln Leu Leu Leu Thr Glu  
465 470 475 480

Gly Pro His Leu Tyr Tyr Val Asp Pro Val Asn Lys Val Leu Lys Gly  
485 490 495

Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu Ala Lys Asn Phe Lys  
500 505 510

Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr Tyr Leu Met Asp Pro  
515 520 525

Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile Gln Glu Val Trp Arg  
530 535 540

Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln  
545 550 555

<210> 4  
<211> 249  
<212> PRT  
<213> Homo sapiens

<400> 4

Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser Leu Gln  
1 5 10 15

His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu Asp Phe  
20 25 30

Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val Val Leu  
35 40 45

Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile Leu Glu  
50 55 60

Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr Arg Glu  
65 70 75 80

Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys Leu Tyr  
85 90 95

Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser Tyr Ala  
100 105 110

Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser Phe Asp  
115 120 125

Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala Leu Glu  
130 135 140

Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn  
145 150 155 160

Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe Gly Thr  
165 170 175

Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn Ser Phe  
180 185 190

Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu Lys Ser  
195 200 205

Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile Tyr Gln  
210 215 220

Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr Leu Ile  
225 230 235 240

Phe Gln Lys Ile Ile Lys Leu Glu Tyr  
245



<211> 8  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Phosphorylation consensus motif

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<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> Any amino acid

<400> 5

Thr Phe Cys Gly Thr Xaa Glu Leu  
1 5

<210> 6  
<211> 229  
<212> PRT  
<213> Homo sapiens

<400> 6

Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu Asp Phe Lys Phe Gly Lys  
1 5 10 15

Ile Leu Gly Glu Gly Ser Phe Ser Thr Val Val Leu Ala Arg Glu Leu  
20 25 30

Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile Leu Glu Lys Arg His Ile  
35 40 45

Ile Lys Glu Asn Lys Val Pro Tyr Val Thr Arg Glu Arg Asp Val Met  
50 55 60

Ser Arg Leu Asp His Pro Phe Phe Val Lys Leu Tyr Phe Thr Phe Gln  
65 70 75 80

Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser Tyr Ala Lys Asn Gly Glu  
85 90 95

Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser Phe Asp Glu Thr Cys Thr  
100 105 110

Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala Leu Glu Tyr Leu His Gly  
115 120 125

Lys Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asn  
130 135 140

Glu Asp Met His Ile Gln Ile Thr Asp Phe Gly Thr Ala Lys Val Leu  
145 150 155 160

Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn Ser Phe Val Gly Thr Ala  
165 170 175

Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu Lys Ser Ala Cys Lys Ser  
180 185 190

Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile Tyr Gln Leu Val Ala Gly  
195 200 205

Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr Leu Ile Phe Gln Lys Ile  
210 215 220

Ile Lys Leu Glu Tyr  
225

<210> 7  
<211> 251  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Modified PDK1

<400> 7

Gly Pro Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser  
1 5 10 15

Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu  
20 25 30

Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val  
35 40 45

Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile  
50 55 60

Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr  
65 70 75 80

Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys  
85 90 95

Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser  
100 105 110

Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser  
115 120 125

Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala  
130 135 140

Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro  
145 150 155 160

Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe  
165 170 175

Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn  
180 185 190

Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu  
195 200 205

Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile  
210 215 220

Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr  
225 230 235 240

Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr  
245 250

<210> 8  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 8

Lys Val Pro Tyr Val Thr Arg Glu Arg Asp Val Met Ser Arg  
1 5 10

<210> 9  
<211> 8  
<212> PRT  
<213> Artificial Sequence

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<223> PDK1 activity

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<221> MISC\_FEATURE  
<222> (1)..(1)  
<223> T or S

<220>  
<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> Any residue

<400> 9

Xaa Phe Cys Gly Thr Xaa Glu Leu  
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<210> 10  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> PDK2 activity

<220>  
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<222> (2)..(3)  
<223> Any residue

<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> S or T

<220>  
<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> P or Y

<400> 10

Pro Xaa Xaa Pro Xaa Xaa  
1 5

<210> 11  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Phosphorylated hydrophobic motif

<220>  
<221> MISC\_FEATURE  
<222> (2)..(3)  
<223> Any residue

<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> Any negatively charged residue

<400> 11

Phe Xaa Xaa Phe Xaa Tyr  
1 5

<210> 12  
<211> 51  
<212> PRT  
<213> Homo sapiens

<400> 12

Gln Pro Arg Lys Lys Arg Pro Glu Asp Phe Lys Phe Gly Lys Ile Leu  
1 5 10 15

Gly Glu Gly Ser Phe Ser Thr Val Val Leu Arg Glu Arg Asp Val Met  
20 25 30

Ser Arg Leu Asp His Pro Phe Phe Val Lys Leu Tyr Phe Thr Phe Gln  
35 40 45

Asp Asp Glu  
50

<210> 13  
<211> 51  
<212> PRT  
<213> Homo sapiens

<400> 13

Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu  
1 5 10 15

Gly Lys Gly Thr Phe Gly Lys Val Ile Leu Thr Glu Asn Arg Val Leu  
20 25 30

Gln Asn Ser Arg His Pro Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln  
35 40 45

Thr His Asp  
50

<210> 14  
<211> 51  
<212> PRT  
<213> Homo sapiens

<400> 14

Gly Pro Glu Lys Ile Arg Pro Glu Cys Phe Glu Leu Leu Arg Val Leu  
1 5 10 15

Gly Lys Gly Gly Tyr Gly Lys Val Phe Gln Ala Glu Arg Asn Ile Leu  
20 25 30

Glu Glu Val Lys His Pro Phe Ile Val Asp Leu Ile Tyr Ala Phe Gln  
35 40 45

Thr Gly Gly  
50

<210> 15  
<211> 52  
<212> PRT  
<213> Homo sapiens

<400> 15

Ser Asn Pro His Ala Lys Pro Ser Asp Phe His Phe Leu Lys Val Ile  
1 5 10 15

Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Ser Glu Arg Asn Val Leu  
20 25 30

Leu Lys Asn Val Lys His Pro Phe Leu Val Gly Leu His Phe Ser Phe  
35 40 45

Gln Thr Ala Asp  
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<210> 16  
<211> 51  
<212> PRT  
<213> Homo sapiens

<400> 16

Gly Ser Glu Lys Ala Asp Pro Ser His Phe Glu Leu Leu Lys Val Leu  
1 5 10 15

Gly Gln Gly Ser Phe Gly Lys Val Phe Leu Met Glu Arg Asp Ile Leu  
20 25 30

Ala Asp Val Asn His Pro Phe Val Val Lys Leu His Tyr Ala Phe Gln  
35 40 45

Thr Glu Gly  
50

<210> 17  
<211> 318  
<212> PRT  
<213> Homo sapiens

<400> 17

Lys Val Phe Gln Val Arg Lys Val Thr Gly Ala Asn Thr Gly Lys Ile  
1 5 10 15

Phe Ala Met Lys Val Leu Lys Lys Ala Met Ile Val Arg Asn Ala Lys  
20 25 30

Asp Thr Ala His Thr Lys Ala Glu Arg Asn Ile Leu Glu Glu Val Lys  
35 40 45

His Pro Phe Ile Val Asp Leu Ile Tyr Ala Phe Gln Thr Gly Gly Lys  
50 55 60

Leu Tyr Leu Ile Leu Glu Tyr Leu Ser Gly Gly Glu Leu Phe Met Gln  
65 70 75 80

Leu Glu Arg Glu Gly Ile Phe Met Glu Asp Thr Ala Cys Phe Tyr Leu  
85 90 95

Ala Glu Ile Ser Met Ala Leu Gly His Leu His Gln Lys Gly Ile Ile  
100 105 110

Tyr Arg Asp Leu Lys Pro Glu Asn Ile Met Leu Asn His Gln Gly His  
115 120 125

Val Lys Leu Thr Asp Phe Gly Leu Cys Lys Glu Ser Ile His Asp Gly  
130 135 140

Thr Val Thr His Thr Phe Cys Gly Thr Ile Glu Tyr Met Ala Pro Glu  
145 150 155 160

Ile Leu Met Arg Ser Gly His Asn Arg Ala Val Asp Trp Trp Ser Leu  
165 170 175

Gly Ala Leu Met Tyr Asp Met Leu Thr Gly Ala Pro Pro Phe Thr Gly  
180 185 190